

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,121

DATE: 10/11/2001

TIME: 09:54:28

Input Set : A:\JH98K008.APP.txt

Output Set: N:\CRF3\10112001\I701121.raw

3 <110> APPLICANT: Hoechst Marion Roussel  
 5 <120> TITLE OF INVENTION: Novel monomer protein with bone morphogenetic activity  
 6 and medicinal agent containing the same for preventing  
 7 and treating diseases of cartilage and bone.  
 9 <130> FILE REFERENCE: JH98K008 PCT SEQUENCES IN ENGLISH  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/701,121 *OK*  
 C--> 12 <141> CURRENT FILING DATE: 2000-11-20  
 14 <150> PRIOR APPLICATION NUMBER: 10-141379  
 15 <151> PRIOR FILING DATE: 1998-05-22  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 357  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: HUMAN  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)..(357) *OK*  
 29 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO 1 from 1  
 30 to 82 and from 84 to 119 in WO 95/04819.  
 31 Note : aminoacid residue 83 is alanine *OK*  
 32 instead of cysteine.  
 34 <300> PUBLICATION INFORMATION:  
 35 <301> AUTHORS: HOTTEN, Gertrud  
 36 NEIDHARDT, Helge  
 37 PAULISTA, Michael  
 38 <302> TITLE: New growth/differentiation factor of the tgfbeta  
 39 familie.  
 40 <310> PATENT DOC NO: WO 95/04819  
 41 <311> PATENT FILING DATE: 1995-02-16 *OK*  
 43 <400> SEQUENCE: 1  
 44 cca cta gca act cgt cag ggc aag cga ccc agc aag aac ctt aag gct 48  
 45 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala  
 46 1 5 10 15  
 48 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg 96  
 49 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp  
 50 20 25 30  
 52 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag 144  
 53 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu  
 54 35 40 45  
 56 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat 192  
 57 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His  
 58 50 55 60  
 60 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca 240  
 61 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro  
 62 65 70 75 80  
 64 ccc acc gcc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc 288

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65 Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
66      85      90      95
68 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc 336
69 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
70      100      105      110
72 gtg gag tcg tgt ggc tgt agg 357
73 Val Glu Ser Cys Gly Cys Arg
74      115
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 119
79 <212> TYPE: PRT
80 <213> ORGANISM: HUMAN
82 <400> SEQUENCE: 2
83 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
84 1      5      10      15
86 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
87      20      25      30
89 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
90      35      40      45
92 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
93      50      55      60
95 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
96 65      70      75      80
98 Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
99      85      90      95
101 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
102      100      105      110
104 Val Glu Ser Cys Gly Cys Arg
105      115
108 <210> SEQ ID NO: 3
109 <211> LENGTH: 39
110 <212> TYPE: DNA
111 <213> ORGANISM: HUMAN
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: (1)..(39) OK
116 <223> OTHER INFORMATION: Sense PCR primer for mutation introducing.
118 <400> SEQUENCE: 3
119 catgccatgg accccgagtc cacaccaccc accgcctgt 39
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 37
124 <212> TYPE: DNA
125 <213> ORGANISM: HUMAN
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: Complement((1)..(37)) OK
130 <223> OTHER INFORMATION: Reverse PCR primer for mutation introducing.
132 <400> SEQUENCE: 4
133 cccaagcttg catgcctgcc ggctcgactac ctacagc 37

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date